

O'Bryen, Barbara

From: Switzer, Juliet
Sent: Wednesday, February 09, 2005 4:05 PM
To: O'Bryen, Barbara
Subject: FW: please search

here's the sequence of I want searched:

aaatgctctgtrtatatgctataagc

the case is CRFE but not in ABSS b/c the CRF is too big. you'd have to go get the CD from mark spencer, but I've already OCR'd the sequence.
thanks.

-----Original Message-----

From: Switzer, Juliet
Sent: Wednesday, February 09, 2005 3:42 PM
To: O'Bryen, Barbara
Subject: please search

please search nucleotides 191-220 of seq id no 1 from 09/925065 in genseq and uspat issued and published.

results on paper is fine

thanks.

J

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phone: 571-272-753
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Ref #	Hits	Search Query	DBs	Default Operator	Plurals	Time Stamp
L1	146	(thiopurine with methyltransferase) or tpmt	US-PGPUB; USPAT	OR	ON	2005/02/09 15:42
L2	54	l1 same (mutation polymorphism snp)	US-PGPUB; USPAT	OR	ON	2005/02/09 15:34
L3	4	l2 same intron\$3	US-PGPUB; USPAT	OR	ON	2005/02/09 15:34
L4	12	(thiopurine with methyltransferase) or tpmt	DERWENT	OR	ON	2005/02/09 15:42

(FILE 'HOME' ENTERED AT 13:36:40 ON 09 FEB 2005)

STN¹

FILE 'MEDLINE, BIOSIS, CAPLUS' ENTERED AT 13:36:48 ON 09 FEB 2005

L1 1317 S THIOPURINE(3A)METHYLTRANSFERASE
L2 928 S TPMT
L3 537 S (L1 OR L2) (4A) (POLYMORPH? OR SNP OR ALLEL?)
L4 6 S L3(6A) (INTRON?)
L5 3 DUP REM L4 (3 DUPLICATES REMOVED)

FILE 'STNGUIDE' ENTERED AT 13:40:29 ON 09 FEB 2005

L6 0 S L3 AND (ADENINE OR GUANINE)

FILE 'MEDLINE, BIOSIS, CAPLUS' ENTERED AT 14:19:38 ON 09 FEB 2005

L7 15 S L6
L8 12 DUP REM L7 (3 DUPLICATES REMOVED)



results of BLAST

BLASTN 2.2.10 [Oct-19-2004]

RID: 1107966805-21412-170660323395.BLASTQ4

Blast Seq ID 1
against dbSNP

Database: human_snp

10,022,444 sequences; 11,321,078,719 total letters

If you have any problems or questions with the results of this search
please refer to the [BLAST FAQs](#)

Taxonomy reports

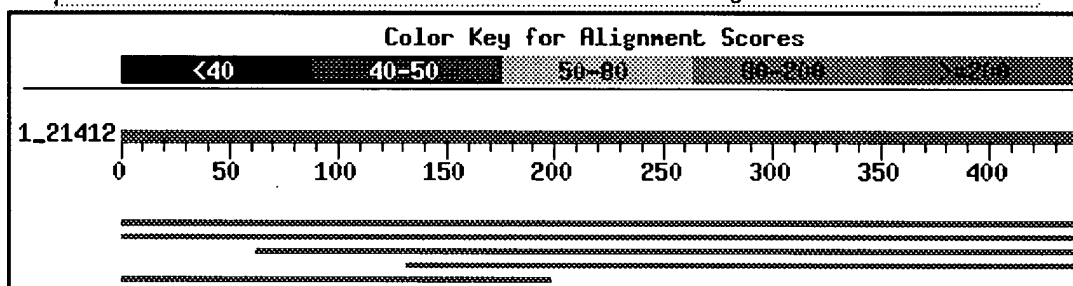
No hits in prior art.

Query=

(440 letters)

Distribution of 5 Blast Hits on the Query Sequence

Mouse-over to show define and scores. Click to show alignments



Sequences producing significant alignments:

Score E
(bits) Value

gnl dbSNP rs3925948	allelePos=205totallen=440;taxid=9606;sn...	845	0.0
gnl dbSNP rs13216460	allelePos=501totallen=941;taxid=9606;s...	837	0.0
gnl dbSNP rs2842946	allelePos=405totallen=605;taxid=9606;sn...	724	0.0
gnl dbSNP rs9367980	allelePos=500totallen=1000;taxid=9606;s...	587	e-165
gnl dbSNP rs9465101	allelePos=151totallen=512;taxid=9606;sn...	375	e-101

Alignments

>gnl|dbSNP|rs3925948 allelePos=205totallen=440;taxid=9606;snpClass=1;alleles='A/G';m
enomic;build=111
Length = 440

bad date

Score = 845 bits (439), Expect = 0.0
Identities = 163/440 (37%)
Strand = Plus / Plus

bad

bad
date

```

Query: 1   ccccccccccccccccccccccccccccccccccccccccccccccccccccccccc 60
          ||
Sbjct: 530 cagagagtgtagttagccaagattgtgccmctgcactccagcgtgggtaacagagtgaga 471

Query: 61   nnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnnn 120
          |||||
Sbjct: 470 ctccatctaaaaaaacacacacacacacacacacacacacacacacacacacacacac 411

```

2/9/05

bad
date

2/9/05

Score = 375 bits (195), Expect = e-101
Identities = 121/199 (60%)
Strand = Plus / Minus

```
Query: 181 ctaatctctgtaaatatgc 199
      |||
Sbjct: 19  ctaatctctgtaaatatgc 1
```

Gapped			
Lambda	K	H	
1.33	0.621		1.12

2/9/05

S2: 25 (48.8 bits)